

AMENDMENTS TO THE SPECIFICATION

Please amend the paragraph [0048] of the published application, on page 14, lines 12-21, to read as follows:

A full length 84P2A9 cDNA clone (clone 1) of 2345 base pairs (SEQ ID NO: 1) was cloned from an LAPC-4 AD cDNA library (Lambda ZAP Express, Stratagene) (FIG. 2). The cDNA encodes an open reading frame (ORF) of 504 amino acids (SEQ ID NO: 2). Sequence analysis revealed the presence of six potential nuclear localization signals and is predicted to be nuclear using the PSORT program (<http://psort.nibb.ac.jp:8800/form.html>). The protein sequence has some homology to a human brain protein KIAA1152 (SEQ ID NO: 5) (39.5% identity over a 337 amino acid region), and contains a domain that is homologous to the LUCA15 tumor suppressor protein (SEQ ID NO: 6) (64.3% identity over a 42 amino acid region) (GenBank Accession #P52756) (FIG. 3).

Please amend the paragraph [0094] of the published application, on page 33, lines 8-18, to read as follows:

As discussed herein, redundancy in the genetic code permits variation in 84P2A9 gene sequences. In particular, one skilled in the art will recognize specific codon preferences by a specific host species, and can adapt the disclosed sequence as preferred for a desired host. For example, preferred analog codon sequences typically have rare codons (i.e., codons having a ~~usage~~ usage frequency of less than about 20% in known sequences of the desired host) replaced with higher frequency codons. Codon preferences for a specific species are calculated, for example, by utilizing codon usage tables available on the INTERNET ~~such as:~~ <http://www.dna.affrc.go.jp/about/nakamura/codon.html>. Nucleotide sequences that have been optimized for a particular host species by replacing any codons having a ~~usage~~ usage frequency of less than about 20% are referred to herein as "codon optimized sequences."

Please amend the paragraph [0100] of the published application, on page 35, line 3 to page 36, line 2, to read as follows:

Illustrating this, the binding of peptides from 84P2A9 proteins to the human MHC class I molecule HLA-A2 were predicted. Specifically, the complete amino acid sequence of the 84P2A9 protein was entered into the HLA Peptide Motif Search algorithm found in the Bioinformatics and Molecular Analysis Section (BIMAS) Web site (<http://bitmas.dortnib.gov/>). The HLA Peptide Motif Search algorithm was developed by Dr. Ken Parker based on binding of specific peptide sequences in the groove of HLA Class I molecules and specifically HLA-A2 (see, e.g., Falk et al. Nature 351: 290-6 (1991); Hunt et al., Science 255:1261-3 (1992); Parker et al., J. Immunol. 149:3580-7 (1992); Parker et al., J. Immunol. 152:163-75 (1994)). This algorithm allows location and ranking of 8-mer, 9-mer, and 10-mer peptides from a complete protein sequence for predicted binding to HLA-A2 as well as numerous other HLA Class I molecules. Many HLA class I binding peptides are 8-, 9-, 10 or 11-mers. For example, for class I HLA-A2, the epitopes preferably contain a leucine (L) or methionine (M) at position 2 and a valine (V) or leucine (L) at the C-terminus (see, e.g., Parker et al., J. Immunol. 149:3580-7 (1992)). Selected results of 84P2A9 predicted binding peptides are shown in Table 1 below. It is to be appreciated that every epitope predicted by the ~~DIMAS~~ BIMAS site, or specified by the HLA class I or class I motifs available in the art are to be applied (e.g., visually or by computer based methods, or appreciated by those of skill in the relevant art) or which become part of the art are within the scope of the invention. In Table 1, the top 10 ranking candidates for each family member are shown along with their location, the amino acid sequence of each specific peptide, and an estimated binding score. The binding score corresponds to the estimated half-time of dissociation of complexes containing the peptide at 37°C at pH 6.5. Peptides with the highest binding score (i.e. 63.04 for 84P2A9) are predicted to be the most tightly bound to HLA Class I on the cell surface for the greatest period of time and thus represent the best immunogenic targets for T-cell recognition. Actual binding of peptides to an HLA allele can be evaluated by stabilization of HLA expression on the antigen-processing defective cell line T2 (see, e.g., Xue et al., Prostate 30:73-8 (1997) and Peshwa et al., Prostate 36:129-38 (1998)). Immunogenicity of specific peptides can be evaluated in vitro by stimulation of CD8+ cytotoxic T lymphocytes (CTL) in the presence of antigen presenting cells such as dendritic cells.

Please amend the paragraph [0207] of the published application, on page 68, lines 10-20, to read as follows:

Genetic immunization methods can be employed to generate prophylactic or therapeutic humoral and cellular immune responses directed against cancer cells expressing 84P2A9. Constructs comprising DNA encoding an 84P2A9-related protein/immunogen and appropriate regulatory sequences can be injected directly into muscle or skin of an individual, such that the cells of the muscle or skin take-up the construct and express the encoded 84P2A9 protein/immunogen. Alternatively, a vaccine comprises an 84P2A9-related protein. Expression of the 84P2A9 protein immunogen results in the generation of prophylactic or therapeutic humoral and cellular immunity against bone, colon, pancreatic, testicular, cervical and ovarian cancers. Various prophylactic and therapeutic genetic immunization techniques known in the art can be used (~~for review, see information and references published at Internet address www.genweb.com~~).

Please amend the paragraph [0235] of the published application, on page 74, lines 8-18, to read as follows:

To determine expression levels of the 84P2A9 gene, 5 μ l of normalized first strand cDNA can be analyzed by PCR using 25, 30, and 35 cycles of amplification using primer pairs that can be designed with the assistance of an MIT genome web site. (~~MIT; for details, see, www.genome.wi.mit.edu~~).

Please amend the paragraph [0241] of the published application, on page 74, lines 28 to page 75, line 8, to read as follows:

A full length 84P2A9 cDNA clone (clone 1) of 2347 base pairs (bp) was cloned from an LAPC-4 AD cDNA library (Lambda ZAP Express, Stratagene) (FIG. 2). The cDNA encodes an open reading frame (ORF) of 504 amino acids. Sequence analysis revealed the presence of six potential nuclear localization signals and is predicted to be nuclear using the PSORT program available on the internet (<http://psortnibb.ac.jp:8800/form.html>). The protein sequence is homologous to a human brain protein KIAA1152 (39.5% identity over a 337 amino acid region), and exhibits a domain that is homologous to the LUCA15 tumor suppressor protein (64.3% identity over a 42 amino acid region)(GenBank Accession #P52756)(FIG. 3). The 84P2A9 cDNA was

deposited on Jan. 5, 2000 with the American Type Culture Collection (ATCC; Manassas, Va.) as plasmid p84P2A9-1, and has been assigned Accession No. PTA-1151.

Please amend the paragraph [0266] of the published application, on page 80, lines 9-13, to read as follows:

The resulting mapping vector for the 93 radiation hybrid panel DNAs was:

00001000110010110010000011000100100100001000101001100010000000100100- 10010
10000000100000010000. This vector and the MIT genome mapping program at <http://www-genome.wi.mit.edu/cgi-bin/contig/rhmapper.pl> placed 84P2A9 on chromosome 1q32.3 (D1S1602-D1S217).